

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: TANABE, Tadashi
- (ii) TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 - (B) STREET: 2100 Pennsylvania Avenue, N.W.
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20037
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/578,709
 - (B) FILING DATE: 28-DEC-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/JP95/00838
 - (B) FILING DATE: 27-APR-1995
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 114316/1994
 - (B) FILING DATE: 28-APR-1994
- (ix) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Gubinsky, Louis
 - (B) REGISTRATION NUMBER: 24,835
 - (C) REFERENCE/DOCKET NUMBER: Q40439
- (x) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202)293-7060
 - (B) TELEFAX: (202)293-7860

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER/SYNTETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGACAAGGA CCACAT

16

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER/SYNTETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAAAAGTCGC CTGTGGAAGC

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER/SYNTETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACAGGGCGAC TTTTGACA

18

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER/SYNTETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGCCTGCATC TCCTCTGA

18

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACTCGAGTC GACATCGATT TTTTTTTTTT TTTTT

35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACTCGAGTC GACATCG

17

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CUACUACUAC UAGGCCACGC GTCGACTAGT ACGGGNNNGG NNGGGNNG

48

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) STRAIN: lambda hPGIS141

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGG GAC AAG GAC CAC ATG TGC AGT GTC AAA AGT CGC CTG TGG AAG CTG
Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu

1 5 10 15

48

CTA TCC CCA GCC AGG CTG GCC AGG CGG GCC CAC CGG AGC AAA TGG CTG
Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu

20 25 30

96

GAG AGT TAC CTG CTG CAC CTG GAG GAG ATG GGT GTG TCA GAG GAG ATG
Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met

35 40 45

144

CAG GCA CGG GCC CTG GTG CTG CAG CTG TGG GCC ACA CAG
Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln

50 55 60

183

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu
1 5 10 15

Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu
20 25 30

Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met
35 40 45

Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln
50 55 60

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) STRAIN: pHPGIS36

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 80..790

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 80..790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTACTACTAC TAGGCCACGC GTCGACTAGT ACGGGGGGGG GGGGGGGGGG GCAGCCCCGC 60

CAGCCCCGCC AGCCCCGCG ATG GCT TGG GCC GCG CTC CTC GGC CTC CTG GCC
Met Ala Trp Ala Ala Leu Leu Gly Leu Leu Ala
1 5 10

GCA CTG TTG CTG CTG CTA CTG AGC CGC CGC ACG CGG CGA CCT
Ala Leu Leu Leu Leu Leu Ser Arg Arg Arg Thr Arg Arg Pro
15 20 25

GGT GAG CCT CCC CTG GAC CTG GGC AGC ATC CCC TGG TTG GGG TAT GCC
Gly Glu Pro Pro Leu Asp Leu Gly Ser Ile Pro Trp Leu Gly Tyr Ala
30 35 40

TTG GAC TTT GGA AAA GAT GCT GCC AGC TTC CTC ACG AGG ATG AAG GAG
Leu Asp Phe Gly Lys Asp Ala Ala Ser Phe Leu Thr Arg Met Lys Glu
45 50 55

AAG CAC GGT GAC ATC TTT ACT ATA CTG GTT GGG GGC AGG TAT GTC ACC
Lys His Gly Asp Ile Phe Thr Ile Leu Val Gly Gly Arg Tyr Val Thr
60 65 70 75

GTT CTC CTG GAC CCA CAC TCC TAC GAC GCG GTG GTG TGG GAG CCT CGC
Val Leu Leu Asp Pro His Ser Tyr Asp Ala Val Val Trp Glu Pro Arg
80 85 90

ACC AGG CTC GAC TTC CAT GCC TAT GCC ATC TTC CTC ATG GAG AGG ATT	400
Thr Arg Leu Asp Phe His Ala Tyr Ala Ile Phe Leu Met Glu Arg Ile	
95 100 105	
TTT GAT GTG CAG CTT CCA CAT TAC AGC CCC AGT GAT GAA AAG GCC AGG	448
Phe Asp Val Gln Leu Pro His Tyr Ser Pro Ser Asp Glu Lys Ala Arg	
110 115 120	
ATG AAA CTG ACT CTT CTC GAC AGA GAG CTC CAG GCA CTC ACA GAA GCC	496
Mét Lys Leu Thr Leu Leu His Arg Glu Leu Gln Ala Leu Thr Glu Ala	
125 130 135	
ATG TAT ACC AAC CTC CAT GCA GTG CTG TTG GGC GAT GCT ACA GAA GCA	544
Met Tyr Thr Asn Leu His Ala Val Leu Leu Gly Asp Ala Thr Glu Ala	
140 145 150 155	
GGC AGT GGC TGG CAC GAG ATG GGT CTC CTC GAC TTC TCC TAC AGC TTC	592
Gly Ser Gly Trp His Glu Met Gly Leu Leu Asp Phe Ser Tyr Ser Phe	
160 165 170	
CTG CTC AGA GCC GGC TAC CTG ACT CTT TAC GGA ATT GAG GCG CTG CCA	640
Leu Leu Arg Ala Gly Tyr Leu Thr Leu Tyr Gly Ile Glu Ala Leu Pro	
175 180 185	
CGC ACC CAT GAA AGC CAG GCC CAG GAC CGC GTC CAC TCA GCT GAT GTC	688
Arg Thr His Glu Ser Gln Ala Gln Asp Arg Val His Ser Ala Asp Val	
190 195 200	
TTC CAC ACC TTT CGC CAG CTC GAC CGG CTG CTC CCC AAA CTG GCC CGT	736
Phe His Thr Phe Arg Gln Leu Asp Arg Leu Leu Pro Lys Leu Ala Arg	
205 210 215	
GGC TCC CTG TCA GTG GGG GAC AAG GAC CAC ATG TGC AGT GTC AAA AGT	784
Gly Ser Leu Ser Val Gly Asp Lys Asp His Met Cys Ser Val Lys Ser	
220 225 230 235	
CGC CTG TG	792
Arg Leu	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Trp Ala Ala Leu Leu Gly Leu Leu Ala Ala Leu Leu Leu
 1 5 10 15

Leu Leu Leu Ser Arg Arg Arg Thr Arg Arg Pro Gly Glu Pro Pro Leu

20	25	30
Asp Leu Gly Ser Ile Pro Trp Leu Gly Tyr Ala Leu Asp Phe Gly Lys		
35	40	45
Asp Ala Ala Ser Phe Leu Thr Arg Met Lys Glu Lys His Gly Asp Ile		
50	55	60
Phe Thr Ile Leu Val Gly Gly Arg Tyr Val Thr Val Leu Leu Asp Pro		
65	70	75
His Ser Tyr Asp Ala Val Val Trp Glu Pro Arg Thr Arg Leu Asp Phe		
85	90	95
His Ala Tyr Ala Ile Phe Leu Met Glu Arg Ile Phe Asp Val Gln Leu		
100	105	110
Pro His Tyr Ser Pro Ser Asp Glu Lys Ala Arg Met Lys Leu Thr Leu		
115	120	125
Leu His Arg Glu Leu Gln Ala Leu Thr Glu Ala Met Tyr Thr Asn Leu		
130	135	140
His Ala Val Leu Leu Gly Asp Ala Thr Glu Ala Gly Ser Gly Trp His		
145	150	155
Glu Met Gly Leu Leu Asp Phe Ser Tyr Ser Phe Leu Leu Arg Ala Gly		
165	170	175
Tyr Leu Thr Leu Tyr Gly Ile Glu Ala Leu Pro Arg Thr His Glu Ser		
180	185	190
Gln Ala Gln Asp Arg Val His Ser Ala Asp Val Phe His Thr Phe Arg		
195	200	205
Gln Leu Asp Arg Leu Leu Pro Lys Leu Ala Arg Gly Ser Leu Ser Val		
210	215	220
Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) STRAIN: pHPGIS135

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 3..827

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 3..827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GG GAC AAG GAC CAC ATG TGC AGT GTC AAA AGT CGC CTG TGG AAG CTG Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu	47
1 5 10 15	
CTA TCC CCA GCC AGG CTG GCC AGG CGG GCC CAC CGG AGC AAA TGG CTG Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu	95
20 25 30	
GAG AGT TAC CTG CTG CAC CTG GAG GAG ATG GGT GTG TCA GAG GAG ATG Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met	143
35 40 45	
CAG GCA CGG GCC CTG GTG CTG CAG CTG TGG GCC ACA CAG GGG AAT ATG Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln Gly Asn Met	191
50 55 60	
GGT CCC GCT GCC TTC TGG CTC CTG CTC TTC CTT CTC AAG AAT CCT GAA Gly Pro Ala Ala Phe Trp Leu Leu Phe Leu Leu Lys Asn Pro Glu	239
65 70 75	
GCC CTG GCT GTC CGC GGA GAG CTC GAG AGT ATC CTT TGG CAA GCG Ala Leu Ala Ala Val Arg Gly Glu Leu Glu Ser Ile Leu Trp Gln Ala	287
80 85 90 95	
GAG CAG CCT GTC TCG CAG ACG ACC ACT CTC CCA CAG AAG GTT CTA GAC Glu Gln Pro Val Ser Gln Thr Thr Leu Pro Gln Lys Val Leu Asp	335
100 105 110	
AGC ACA CCT GTG CTT GAT AGC GTG CTG AGT GAG AGC CTC AGG CTT ACA Ser Thr Pro Val Leu Asp Ser Val Leu Ser Glu Ser Leu Arg Leu Thr	383
115 120 125	
GCT GCC CCC TTC ATC ACC CGC GAG GTT GTG GTG GAC CTG GCC ATG CCC Ala Ala Pro Phe Ile Thr Arg Glu Val Val Val Asp Leu Ala Met Pro	431
130 135 140	
ATG GCA GAC GGG AGA GAA TTC AAC CTG CGA CGT GGT GAC CGC CTC CTC Met Ala Asp Gly Arg Glu Phe Asn Leu Arg Arg Gly Asp Arg Leu Leu	479
145 150 155	
CTC TTC CCC TTC CTG AGC CCC CAG AGA GAC CCA GAA ATC TAC ACA GAC Leu Phe Pro Phe Leu Ser Pro Gln Arg Asp Pro Glu Ile Tyr Thr Asp	527
160 165 170 175	
CCA GAG GTA TTT AAA TAC AAC CGA TTC CTG AAC CCT GAC GGA TCA GAG Pro Glu Val Phe Lys Tyr Asn Arg Phe Leu Asn Pro Asp Gly Ser Glu	575
180 185 190	

AAG AAA GAC TTT TAC AAG GAT GGG AAA CGG CTG AAG AAT TAC AAC ATG Lys Lys Asp Phe Tyr Lys Asp Gly Lys Arg Leu Lys Asn Tyr Asn Met 195 200 205	623
CCC TGG GGG GCG GGG CAC AAT CAC TGC CTG GGG AGG AGT TAT GCG GTC Pro Trp Gly Ala Gly His Asn His Cys Leu Gly Arg Ser Tyr Ala Val 210 215 220	671
AAC AGC ATC AAA CAA TTT GTG TTC CTT GTG CTG GTG CAC TTG GAC TTG Asn Ser Ile Lys Gln Phe Val Phe Leu Val Leu Val His Leu Asp Leu 225 230 235	719
GAG CTG ATC AAC GCA GAT GTG GAG ATC CCT GAG TTT GAC CTC AGC AGG Glu Leu Ile Asn Ala Asp Val Glu Ile Pro Glu Phe Asp Leu Ser Arg 240 245 250 255	767
TAC GGC TTC GGT CTG ATG CAG CCG GAA CAC GAC GTG CCC GTC CGC TAC Tyr Gly Phe Gly Leu Met Gln Pro Glu His Asp Val Pro Val Arg Tyr 260 265 270	815
CGC ATC CGC CCA TGACACAGGG AGCAGATGGA TCCACGTGCT CGCCTCTGCC Arg Ile Arg Pro 275	867
CAGCCTGCC CAGCCTGCC CAGCCTCCA GCTTCTGTG TGACAGTTG GCCCGGTGC	927
AGGTGCTAGC ATTACCACTT CCCTGCTTT CTCCCAGAAG GCTGGGTCCA GGGAGGGAA	987
AAGCTAACAG GGTGAACAAA GAAAAGACAT TGAAAGCTCT ATGGATTATC CACTGCAAAG	1047
TTTCTTCC AAAATCAGGC TTTGTCTGCT CCCAATTACAC CTCGTTACTC TCACCTCGTG	1107
ATATCCACAA ATGCTATTCA GATAAGGCAG AACTAGGAGT CTTCACTGCT CTGCCCCCAA	1167
CTCCCGGAGG TGTCACCTTC CTAGTTCTTA TGAGCTAGCA TGGCCCGGGC CTTATCCAGT	1227
CAAAGCGGAT GCTGGCCACA GAAAGGCCAC TCAGGATGTC CTTTGTGTCC ATCGATGTCG	1287
ACTCGAGTC	1296

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu Leu
1 5 10 15

Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu Glu
20 25 30

Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met Gln
 35 40 45

Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln Gly Asn Met Gly
 50 55 60

Pro Ala Ala Phe Trp Leu Leu Leu Phe Leu Lys Asn Pro Glu Ala
 65 70 75 80

Leu Ala Ala Val Arg Gly Glu Leu Glu Ser Ile Leu Trp Gln Ala Glu
 85 90 95

Gln Pro Val Ser Gln Thr Thr Leu Pro Gln Lys Val Leu Asp Ser
 100 105 110

Thr Pro Val Leu Asp Ser Val Leu Ser Glu Ser Ile Arg Leu Thr Ala
 115 120 125

Ala Pro Phe Ile Thr Arg Glu Val Val Val Asp Leu Ala Met Pro Met
 130 135 140

Ala Asp Gly Arg Glu Phe Asn Leu Arg Arg Gly Asp Arg Leu Leu Leu
 145 150 155 160

Phe Pro Phe Leu Ser Pro Gln Arg Asp Pro Glu Ile Tyr Thr Asp Pro
 165 170 175

Glu Val Phe Lys Tyr Asn Arg Phe Leu Asn Pro Asp Gly Ser Glu Lys
 180 185 190

Lys Asp Phe Tyr Lys Asp Gly Lys Arg Leu Lys Asn Tyr Asn Met Pro
 195 200 205

Trp Gly Ala Gly His Asn His Cys Leu Gly Arg Ser Tyr Ala Val Asn
 210 215 220

Ser Ile Lys Gln Phe Val Phe Leu Val Leu His Leu Asp Leu Glu
 225 230 235 240

Leu Ile Asn Ala Asp Val Glu Ile Pro Glu Phe Asp Leu Ser Arg Tyr
 245 250 255

Gly Phe Gly Leu Met Gln Pro Glu His Asp Val Pro Val Arg Tyr Arg
 260 265 270

Ile Arg Pro
 275

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1977 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 28..1527

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 28..1527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGCCCCGCCA	GCCCCGCCAG	CCCCGCG	ATG GCT TGG GCC GCG CTC CTC GGC	51
Met Ala Trp	Ala Ala Leu Leu Gly			
1			5	
CTC CTG GCC GCA CTG TTG CTG CTG CTA CTG AGC CGC CGC CGC ACG	99			
Leu Leu Ala Ala Leu Leu Leu Leu Leu Ser Arg Arg Arg Thr				
10	15		20	
CGG CGA CCT GGT GAG CCT CCC CTG GAC CTG GGC AGC ATC CCC TGG TTG	147			
Arg Arg Pro Gly Glu Pro Pro Leu Asp Leu Gly Ser Ile Pro Trp Leu				
25	30	35	40	
GGG TAT GCC TTG GAC TTT GGA AAA GAT GCT GCC AGC TTC CTC ACG AGG	195			
Gly Tyr Ala Leu Asp Phe Gly Lys Asp Ala Ala Ser Phe Leu Thr Arg				
45	50		55	
ATG AAG GAG AAG CAC GGT GAC ATC TTT ACT ATA CTG GTT GGG GGC AGG	243			
Met Lys Glu Lys His Gly Asp Ile Phe Thr Ile Leu Val Gly Gly Arg				
60	65		70	
TAT GTC ACC GTT CTC CTG GAC CCA CAC TCC TAC GAC GCG GTG GTG TGG	291			
Tyr Val Thr Val Leu Leu Asp Pro His Ser Tyr Asp Ala Val Val Trp				
75	80		85	
GAG CCT CGC ACC AGG CTC GAC TTC CAT GCC TAT GCC ATC TTC CTC ATG	339			
Glu Pro Arg Thr Arg Leu Asp Phe His Ala Tyr Ala Ile Phe Leu Met				
90	95		100	
GAG AGG ATT TTT GAT GTG CAG CTT CCA CAT TAC AGC CCC AGT GAT GAA	387			
Glu Arg Ile Phe Asp Val Gln Leu Pro His Tyr Ser Pro Ser Asp Glu				
105	110	115	120	
AAG GCC AGG ATG AAA CTG ACT CTT CTC CAC AGA GAG CTC CAG GCA CTC	435			
Lys Ala Arg Met Lys Leu Thr Leu Leu His Arg Glu Leu Gln Ala Leu				
125	130		135	
ACA GAA GCC ATG TAT ACC AAC CTC CAT GCA GTG CTG TTG GGC GAT GCT	483			
Thr Glu Ala Met Tyr Thr Asn Leu His Ala Val Leu Leu Gly Asp Ala				
140	145		150	
ACA GAA GCA GGC AGT GGC TGG CAC GAG ATG GGT CTC CTC GAC TTC TCC	531			

Thr Glu Ala Gly Ser Gly Trp His Glu Met Gly Leu Leu Asp Phe Ser			
155	160	165	
TAC AGC TTC CTG CTC AGA GCC GGC TAC CTG ACT CTT TAC GGA ATT GAG			579
Tyr Ser Phe Leu Leu Arg Ala Gly Tyr Leu Thr Leu Tyr Gly Ile Glu			
170	175	180	
GCG CTG CCA CGC ACC CAT GAA AGC CAG GCC CAG GAC CGC GTC CAC TCA			627
Ala Leu Pro Arg Thr His Glu Ser Gln Ala Gln Asp Arg Val His Ser			
185	190	195	200
GCT GAT GTC TTC CAC ACC TTT CGC CAG CTC GAC CGG CTG CTC CCC AAA			675
Ala Asp Val Phe His Thr Phe Arg Gln Leu Asp Arg Leu Leu Pro Lys			
205	210	215	
CTG GCC CGT GGC TCC CTG TCA GTG GGG GAC AAG GAC CAC ATG TGC AGT			723
Leu Ala Arg Gly Ser Leu Ser Val Gly Asp Lys Asp His Met Cys Ser			
220	225	230	
GTC AAA AGT CGC CTG TGG AAG CTG CTA TCC CCA GCC AGG CTG GCC AGG			771
Val Lys Ser Arg Leu Trp Lys Leu Leu Ser Pro Ala Arg Leu Ala Arg			
235	240	245	
CGG GCC CAC CGG AGC AAA TGG CTG GAG AGT TAC CTG CTG CAC CTG GAG			819
Arg Ala His Arg Ser Lys Trp Leu Glu Ser Tyr Leu Leu His Leu Glu			
250	255	260	
GAG ATG GGT GTG TCA GAG GAG ATG CAG GCA CGG GCC CTG GTG CTG CAG			867
Glu Met Gly Val Ser Glu Glu Met Gln Ala Arg Ala Leu Val Leu Gln			
265	270	275	280
CTG TGG GCC ACA CAG GGG AAT ATG GGT CCC GCT GCC TTC TGG CTC CTG			915
Leu Trp Ala Thr Gln Gly Asn Met Gly Pro Ala Ala Phe Trp Leu Leu			
285	290	295	
CTC TTC CTT CTC AAG AAT CCT GAA GCC CTG GCT GTC GTC CGC GGA GAG			963
Leu Phe Leu Leu Lys Asn Pro Glu Ala Leu Ala Ala Val Arg Gly Glu			
300	305	310	
CTC GAG AGT ATC CTT TGG CAA GCG GAG CAG CCT GTC TCG CAG ACG ACC			1011
Leu Glu Ser Ile Leu Trp Gln Ala Glu Gln Pro Val Ser Gln Thr Thr			
315	320	325	
ACT CTC CCA CAG AAG GTT CTA GAC AGC ACA CCT GTG CTT GAT AGC GTG			1059
Thr Leu Pro Gln Lys Val Leu Asp Ser Thr Pro Val Leu Asp Ser Val			
330	335	340	
CTG AGT GAG AGC CTC AGG CTT ACA GCT GCC CCC TTC ATC ACC CGC GAG			1107
Leu Ser Glu Ser Leu Arg Leu Thr Ala Ala Pro Phe Ile Thr Arg Glu			
345	350	355	360
GTT GTG GTG GAC CTG GCC ATG CCC ATG GCA GAC GGG AGA GAA TTC AAC			1155
Val Val Val Asp Leu Ala Met Pro Met Ala Asp Gly Arg Glu Phe Asn			
365	370	375	
CTG CGA CGT GGT GAC CGC CTC CTC TTC CCC TTC CTG AGC CCC CAG			1203
Leu Arg Arg Gly Asp Arg Leu Leu Leu Phe Pro Phe Leu Ser Pro Gln			

380	385	390	
AGA GAC CCA GAA ATC TAC ACA GAC CCA GAG GTA TTT AAA TAC AAC CGA Arg Asp Pro Glu Ile Tyr Thr Asp Pro Glu Val Phe Lys Tyr Asn Arg 395	400	405	1251
TTC CTG AAC CCT GAC GGA TCA GAG AAG AAA GAC TTT TAC AAG GAT GGG Phe Leu Asn Pro Asp Gly Ser Glu Lys Lys Asp Phe Tyr Lys Asp Gly 410	415	420	1299
AAA CGG CTG AAG AAT TAC AAC ATG CCC TGG GGG GCG GGG CAC AAT CAC Lys Arg Leu Lys Asn Tyr Asn Met Pro Trp Gly Ala Gly His Asn His 425	430	435	1347
TGC CTG GGG AGG AGT TAT GCG GTC AAC AGC ATC AAA CAA TTT GTG TTC Cys Leu Gly Arg Ser Tyr Ala Val Asn Ser Ile Lys Gln Phe Val Phe 445	450	455	1395
CTT GTG CTG GTG CAC TTG GAC TTG GAG CTG ATC AAC GCA GAT GTG GAG Leu Val Leu Val His Leu Asp Leu Glu Leu Ile Asn Ala Asp Val Glu 460	465	470	1443
ATC CCT GAG TTT GAC CTC AGC AGG TAC GGC TTC GGT CTG ATG CAG CCG Ile Pro Glu Phe Asp Leu Ser Arg Tyr Gly Phe Gly Leu Met Gln Pro 475	480	485	1491
GAA CAC GAC GTG CCC GTC CGC TAC CGC ATC CGC CCA TGACACAGGG Glu His Asp Val Pro Val Arg Tyr Arg Ile Arg Pro 490	495	500	1537
AGCAGATGGA TCCACGTGCT CGCCTCTGCC CAGCCTGCC CAGCCTCCC GCTTCTGTG TGCACAGTTG GCCCGGGTGC AGGTGCTAGC ATTACCACTT CCCTGCTTT			1597
CTCCCAGAAG GCTGGGTCCA GGGGAGGGAA AAGCTAAGAG GGTGAACAAA GAAAAGACAT			1717
TGAAAGCTCT ATGGATTATC CACTGCAAAG TTTCTTTCC AAAATCAGGC TTTGTCTGCT			1777
CCCAATTCAC CTCGTTACTC TCACCTCGTG ATATCCACAA ATGCTATTCA GATAAGGCAG			1837
AACTAGGAGT CTTCACTGCT CTGCCCCCAA CTCCCGGAGG TGTCACCTTC CTAGTTCTTA			1897
TGAGCTAGCA TGGCCCGGGC CTTATCCAGT CAAAGCGGAT GCTGGCCACA GAAAGGCCAC			1957
TCAGGATGTC CTTTGTGTCC			1977

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Trp Ala Ala Leu Leu Gly Leu Leu Ala Ala Leu Leu Leu
1 5 10 15

Leu Leu Leu Ser Arg Arg Arg Thr Arg Arg Pro Gly Glu Pro Pro Leu
20 25 30

Asp Leu Gly Ser Ile Pro Trp Leu Gly Tyr Ala Leu Asp Phe Gly Lys
35 40 45

Asp Ala Ala Ser Phe Leu Thr Arg Met Lys Glu Lys His Gly Asp Ile
50 55 60

Phe Thr Ile Leu Val Gly Gly Arg Tyr Val Thr Val Leu Leu Asp Pro
65 70 75 80

His Ser Tyr Asp Ala Val Val Trp Glu Pro Arg Thr Arg Leu Asp Phe
85 90 95

His Ala Tyr Ala Ile Phe Leu Met Glu Arg Ile Phe Asp Val Gln Leu
100 105 110

Pro His Tyr Ser Pro Ser Asp Glu Lys Ala Arg Met Lys Leu Thr Leu
115 120 125

Leu His Arg Glu Leu Gln Ala Leu Thr Glu Ala Met Tyr Thr Asn Leu
130 135 140

His Ala Val Leu Leu Gly Asp Ala Thr Glu Ala Gly Ser Gly Trp His
145 150 155 160

Glu Met Gly Leu Leu Asp Phe Ser Tyr Ser Phe Leu Leu Arg Ala Gly
165 170 175

Tyr Leu Thr Leu Tyr Gly Ile Glu Ala Leu Pro Arg Thr His Glu Ser
180 185 190

Gln Ala Gln Asp Arg Val His Ser Ala Asp Val Phe His Thr Phe Arg
195 200 205

Gln Leu Asp Arg Leu Leu Pro Lys Leu Ala Arg Gly Ser Leu Ser Val
210 215 220

Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu
225 230 235 240

Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu
245 250 255

Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met
260 265 270

Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln Gly Asn Met
275 280 285

Gly Pro Ala Ala Phe Trp Leu Leu Leu Phe Leu Leu Lys Asn Pro Glu
290 295 300

Ala Leu Ala Ala Val Arg Gly Glu Leu Glu Ser Ile Leu Trp Gln Ala
 305 310 315 320
 Glu Gln Pro Val Ser Gln Thr Thr Leu Pro Gln Lys Val Leu Asp
 325 330 335
 Ser Thr Pro Val Leu Asp Ser Val Leu Ser Glu Ser Leu Arg Leu Thr
 340 345 350
 Ala Ala Pro Phe Ile Thr Arg Glu Val Val Val Asp Leu Ala Met Pro
 355 360 365
 Met Ala Asp Gly Arg Glu Phe Asn Leu Arg Arg Gly Asp Arg Leu Leu
 370 375 380
 Leu Phe Pro Phe Leu Ser Pro Gln Arg Asp Pro Glu Ile Tyr Thr Asp
 385 390 395 400
 Pro Glu Val Phe Lys Tyr Asn Arg Phe Leu Asn Pro Asp Gly Ser Glu
 405 410 415
 Lys Lys Asp Phe Tyr Lys Asp Gly Lys Arg Leu Lys Asn Tyr Asn Met
 420 425 430
 Pro Trp Gly Ala Gly His Asn His Cys Leu Gly Arg Ser Tyr Ala Val
 435 440 445
 Asn Ser Ile Lys Gln Phe Val Phe Leu Val Leu Val His Leu Asp Leu
 450 455 460
 Glu Leu Ile Asn Ala Asp Val Glu Ile Pro Glu Phe Asp Leu Ser Arg
 465 470 475 480
 Tyr Gly Phe Gly Leu Met Gln Pro Glu His Asp Val Pro Val Arg Tyr
 485 490 495
 Arg Ile Arg Pro
 500

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER/SYNTETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GACAAGGACC ACATGTGCAG TGTC

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER/SYNTETIC DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGTGTGGCC CACAGCTGCA GCAC

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